

Background

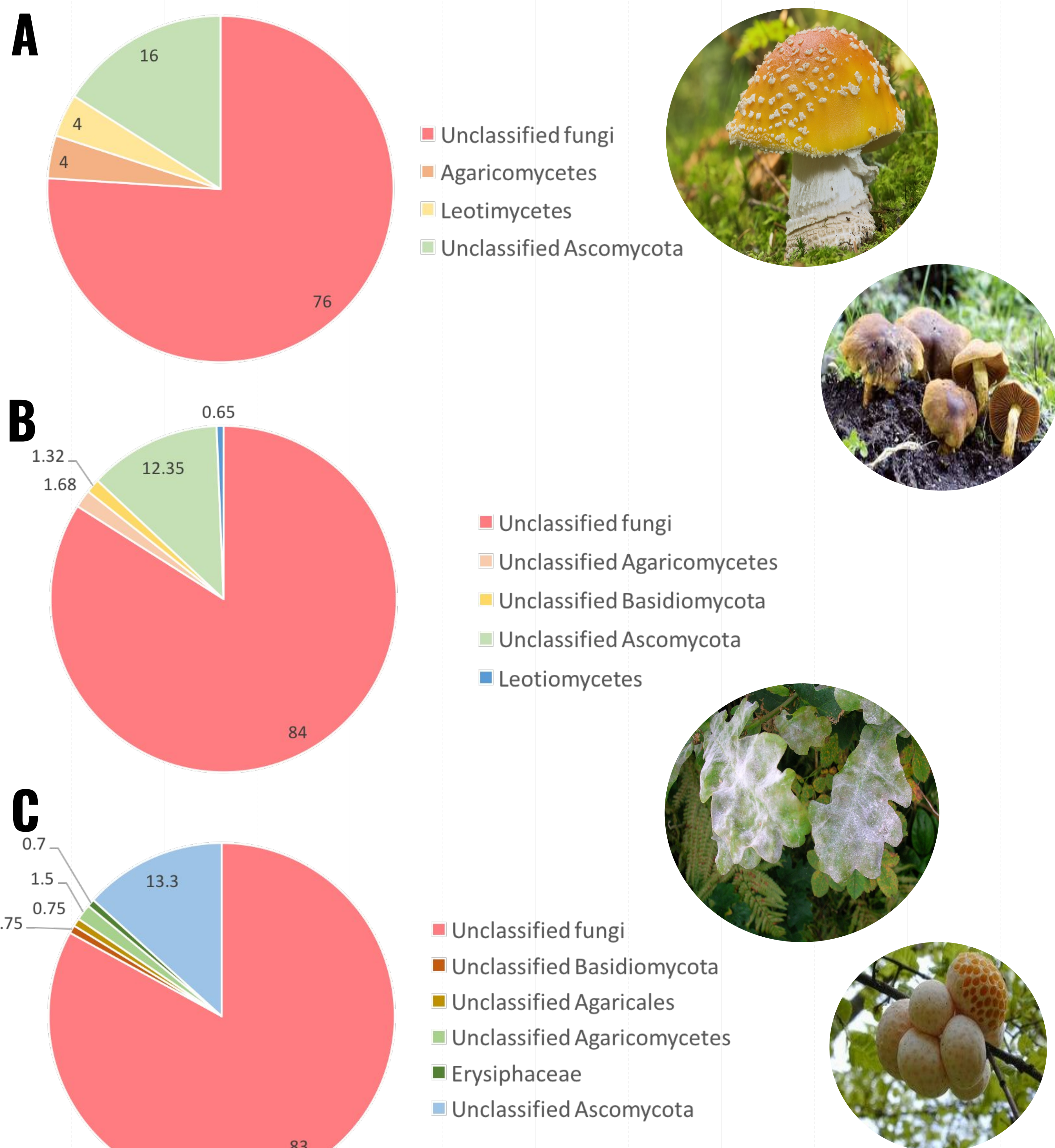
- The chaparral burns every 40-70 years
- Fire affects physical, chemical, and biological processes in the soil
- In May 2014, the Cocos fire burned ~2000 acres of chaparral behind CSUSM
- Post-fire, portions of the burned slope were either hydroseeded or left to recover naturally
- This unique situation allows for analysis of fire effects and post-fire management on belowground fungal communities



Results

Figure 1. Fungal OTU diversity and abundance percentages of the (A) naturally recovering, (B) hydroseeded, and (C) unburned sites.

A majority of fungi remained unclassified. Primary classifications consisted of Basidiomycota and Ascomycota, two common phylum of Fungi. Further classifications of Basidiomycota included Agaricomycetes (a class of cup-shaped fungi) and Agaricales (the common gilled mushroom). Further classifications of Ascomycota included Erysiphaceae (a family of fungi comprised of powdery mildew that is parasitic to leaves of plants) and Leotiomyces, a class of fungi that cause a variety of plant diseases.



Methods

Soil was sampled from transects on unburned, hydroseeded, and naturally recovering sites.



Soil samples were sieved, and subsamples from each plot were pooled together.



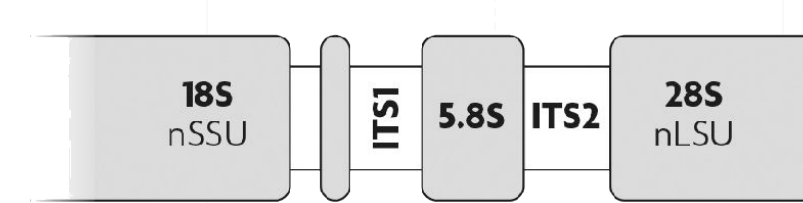
Fungal genomic DNA was extracted from samples using ZymoBIOMICS™ DNA MicroPrep kit.



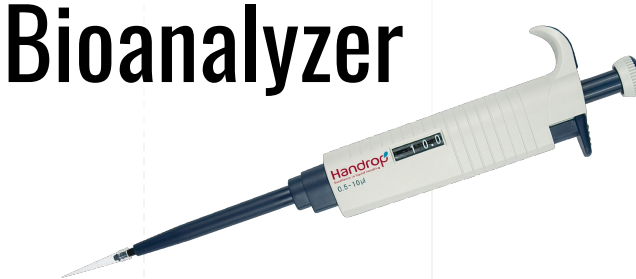
DNA quantity measured with Qubit 2.0 Fluorometer



ITS1 primers (ligated with Illumina adapters) for the ITS region were used to amplify each sample



Libraries were uniquely barcoded using Illumina Nextera® XT indices, cleaned using Agencourt AMPure XP magnetic beads, pooled, and analyzed on an Agilent Bioanalyzer



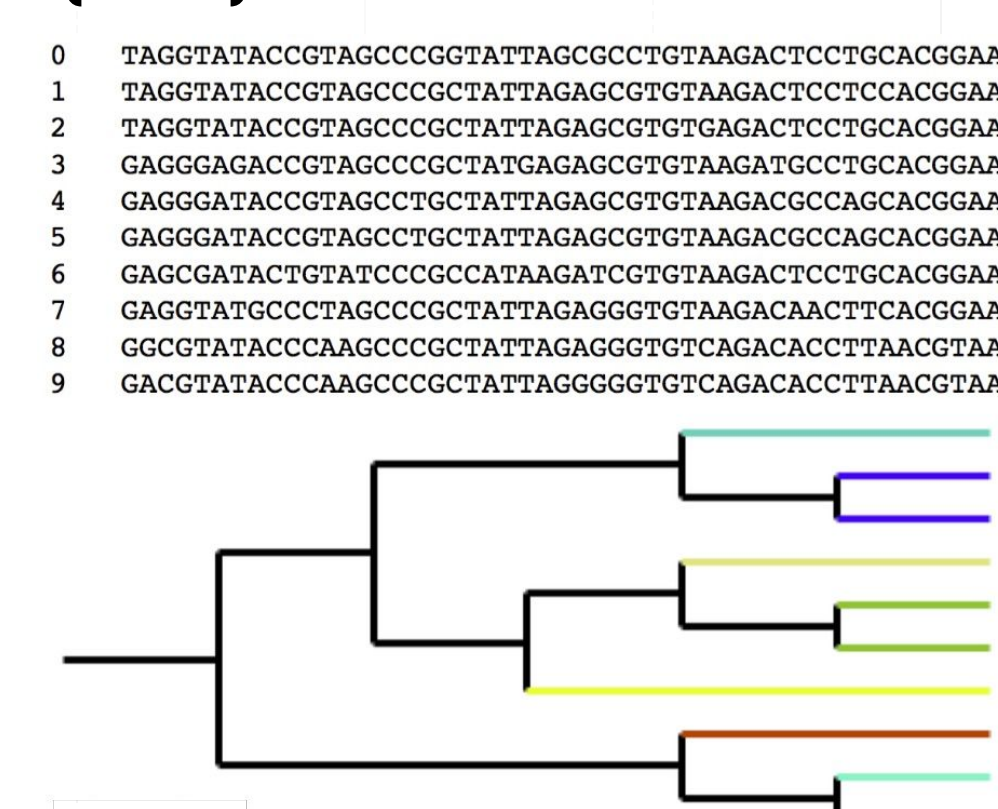
Pooled samples were sequenced on a Illumina MiSeq (150 bp, paired-end) at the UC Riverside Genomics Core



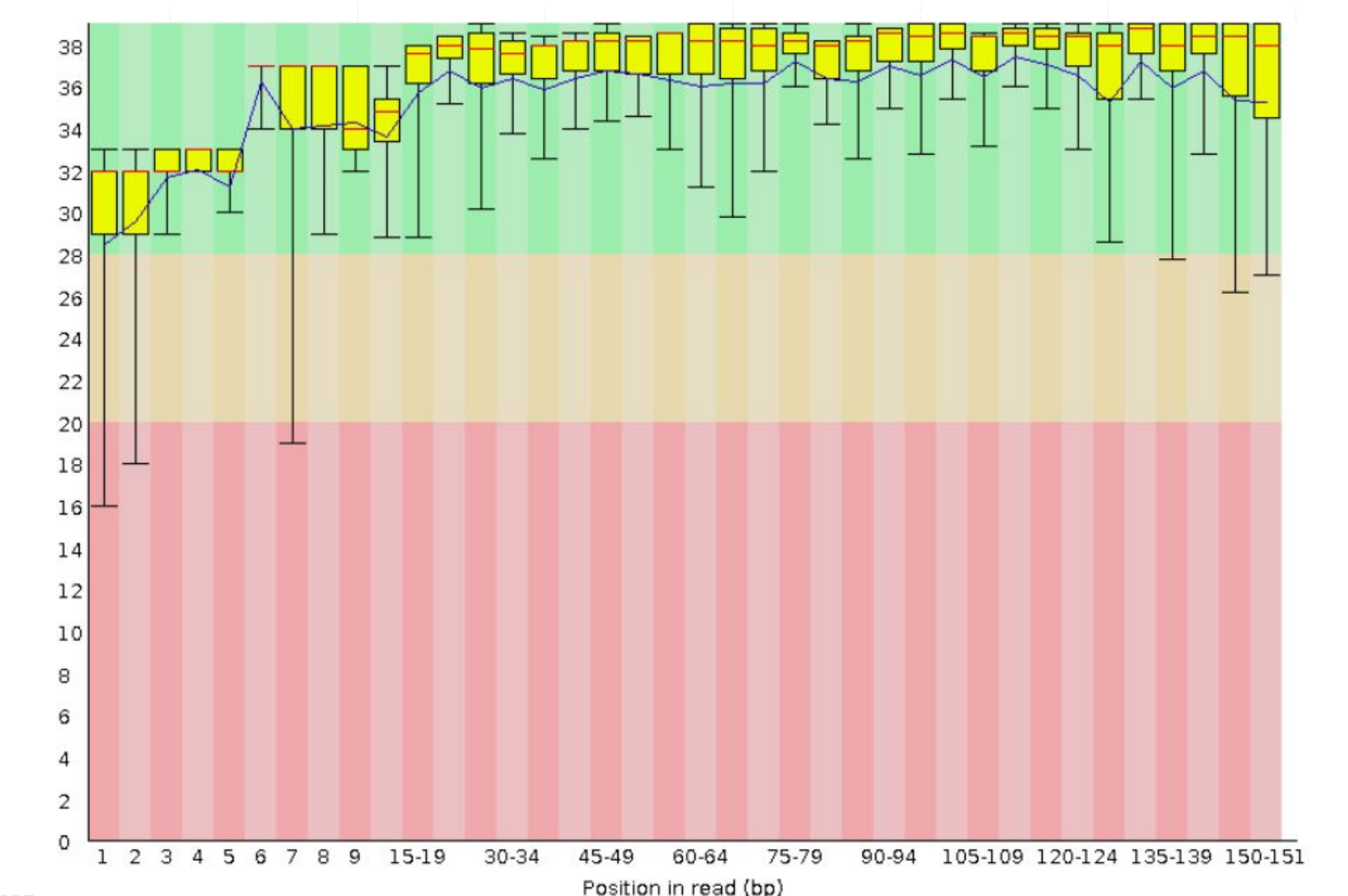
Data Analyzed using the MOTHR pipeline in the Galaxy Project



Findley ITS Database used for Operational Taxonomic Unit (OTU) identification



Base Quality Across Length of Reads Generated Using FastQC



Yield	4.47 GB
% Barcode Match	88.9%
% of Bases with >= Q30	90.99%
Mean Quality Score	35.83
Mean Read Length	150 BP

Future Directions

- OTU classification with larger UNITE database on local machine - memory limitations encountered during classification inside the Galaxy Project
- Perform OTU classification using alignment-based algorithm
- Repeat demultiplexing step - may possibly increase % barcode matching and reduce unclassified data
- Explore other metagenomic pipelines to maximize OTU classification - Qiime2



References

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2. Cooke, Wm Bridge. (1970). Sydowia 24: 164-168.
3. Findley et al. (2013). Nature 7454:367-70
4. Vourlitis et al. (2017). Ecological Engineering 102: 46-54
5. Nilsson et al. (2018). Nucleic Acids Research 47.D1: D295-D264

Acknowledgements

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